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Revised 04/24/2003

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION:  US/10/612,466

DATE: 08/11/2003
TIME: 13:38:59

Input Set : A:\1625seq.001
Output Set: N:\CRF4\08112003\J612466.raw

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 3 <110> APPLICANT: Madison, Edwin
 4        Ong, Edgar
 5        Yeh, Juinn-Chern
 7 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE 16, THE
 8        ENCODED PROTEINS AND METHODS BASED THEREON
10 <130> FILE REFERENCE: 24745-1625
12 <140> CURRENT APPLICATION NUMBER: US/10/612,466
13 <141> CURRENT FILING DATE: 2003-07-01
15 <150> PRIOR APPLICATION NUMBER: 60/394,347
16 <151> PRIOR FILING DATE: 02-JUL-02  2002-07-02
18 <160> NUMBER OF SEQ ID NOS: 22
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3147
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo Sapien
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (23)...(2589)
30 <223> OTHER INFORMATION: Nucleotide sequence encoding MTSP1
32 <300> PUBLICATION INFORMATION:
33 <308> DATABASE ACCESSION NO: GenBank #AR081724
34 <309> DATABASE ENTRY DATE: 2000-08-31
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39                           1               5                  10
41 ggg ggc ccg aag gac ttc ggc gcg gga ctc aag tac aac tcc cgg cac  100
42 Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His
43                15                  20                  25
45 gag aaa gtg aat ggc ttg gag gaa ggc gtg gag ttc ctg cca gtc aac  148
46 Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn
47                30                  35                  40
49 aac gtc aag aag gtg gaa aag cat ggc ccg ggg cgc tgg gtg gtg ctg  196
50 Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu
51                45                  50                  55
53 gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc  244
54 Ala Ala Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe
55        60                  65                  70
57 ctg gtg tgg cat ttg cag tac cgg gac gtg cgt gtc cag aag gtc ttc  292
58 Leu Val Trp His Leu Gln Tyr Arg Asp Val Arg Val Gln Lys Val Phe
59 75                  80                  85                  90
61 aat ggc tac atg agg atc aca aat gag aat ttt gtg gat gcc tac gag  340
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RAW SEQUENCE LISTING        DATE: 08/11/2003
PATENT APPLICATION: **US/10/612,466**    TIME: 13:38:59

Input Set : **A:\1625seq.001**
Output Set: **N:\CRF4\08112003\J612466.raw**

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 62 Asn Gly Tyr Met Arg Ile Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu
 63                 95                100                105
 65 aac tcc aac tcc act gag ttt gta agc ctg gcc agc aag gtg aag gac   388
 66 Asn Ser Asn Ser Thr Glu Phe Val Ser Leu Ala Ser Lys Val Lys Asp
 67                110                115                120
 69 gcg ctg aag ctg ctg tac agc gga gtc cca ttc ctg ggc ccc tac cac   436
 70 Ala Leu Lys Leu Leu Tyr Ser Gly Val Pro Phe Leu Gly Pro Tyr His
 71        125                130                135
 73 aag gag tcg gct gtg acg gcc ttc agc gag ggc agc gtc atc gcc tac   484
 74 Lys Glu Ser Ala Val Thr Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr
 75        140                145                150
 77 tac tgg tct gag ttc agc atc ccg cag cac ctg gtg gag gag gcc gag   532
 78 Tyr Trp Ser Glu Phe Ser Ile Pro Gln His Leu Val Glu Glu Ala Glu
 79 155                160                165                170
 81 cgc gtc atg gcc gag gag cgc gta gtc atg ctg ccc ccg cgg gcg cgc   580
 82 Arg Val Met Ala Glu Glu Arg Val Val Met Leu Pro Pro Arg Ala Arg
 83                175                180                185
 85 tcc ctg aag tcc ttt gtg gtc acc tca gtg gtg gct ttc ccc acg gac   628
 86 Ser Leu Lys Ser Phe Val Val Thr Ser Val Val Ala Phe Pro Thr Asp
 87                190                195                200
 89 tcc aaa aca gta cag agg acc cag gac aac agc tgc agc ttt ggc ctg   676
 90 Ser Lys Thr Val Gln Arg Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu
 91        205                210                215
 93 cac gcc cgc ggt gtg gag ctg atg cgc ttc acc acg ccc ggc ttc cct   724
 94 His Ala Arg Gly Val Glu Leu Met Arg Phe Thr Thr Pro Gly Phe Pro
 95        220                225                230
 97 gac agc ccc tac ccc gct cat gcc cgc tgc cag tgg gcc ctg cgg ggg   772
 98 Asp Ser Pro Tyr Pro Ala His Ala Arg Cys Gln Trp Ala Leu Arg Gly
 99 235                240                245                250
101 gac gcc gac tca gtg ctg agc ctc acc ttc cgc agc ttt gac ctt gcg   820
102 Asp Ala Asp Ser Val Leu Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala
103                255                260                265
105 tcc tgc gac gag cgc ggc agc gac ctg gtg acg gtg tac aac acc ctg   868
106 Ser Cys Asp Glu Arg Gly Ser Asp Leu Val Thr Val Tyr Asn Thr Leu
107                270                275                280
109 agc ccc atg gag ccc cac gcc ctg gtg cag ttg tgt ggc acc tac cct   916
110 Ser Pro Met Glu Pro His Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro
111        285                290                295
113 ccc tcc tac aac ctg acc ttc cac tcc tcc cag aac gtc ctg ctc atc   964
114 Pro Ser Tyr Asn Leu Thr Phe His Ser Ser Gln Asn Val Leu Leu Ile
115        300                305                310
117 aca ctg ata acc aac act gag cgg cgg cat ccc ggc ttt gag gcc acc  1012
118 Thr Leu Ile Thr Asn Thr Glu Arg Arg His Pro Gly Phe Glu Ala Thr
119 315                320                325                330
121 ttc ttc cag ctg cct agg atg agc agc tgt gga ggc cgc tta cgt aaa  1060
122 Phe Phe Gln Leu Pro Arg Met Ser Ser Cys Gly Gly Arg Leu Arg Lys
123                335                340                345
125 gcc cag ggg aca ttc aac agc ccc tac tac cca ggc cac tac cca ccc  1108
126 Ala Gln Gly Thr Phe Asn Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro
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129 aac att gac tgc aca tgg aac att gag gtg ccc aac aac cag cat gtg   1156
130 Asn Ile Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val
131          365              370              375
133 aag gtg agc ttc aaa ttc ttc tac ctg ctg gag ccc ggc gtg cct gcg   1204
134 Lys Val Ser Phe Lys Phe Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala
135          380              385              390
137 ggc acc tgc ccc aag gac tac gtg gag atc aat ggg gag aaa tac tgc   1252
138 Gly Thr Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys
139 395              400              405              410
141 gga gag agg tcc cag ttc gtc gtc acc agc aac agc aac aag atc aca   1300
142 Gly Glu Arg Ser Gln Phe Val Val Thr Ser Asn Ser Asn Lys Ile Thr
143          415              420              425
145 gtt cgc ttc cac tca gat cag tcc tac acc gac acc ggc ttc tta gct   1348
146 Val Arg Phe His Ser Asp Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala
147          430              435              440
149 gaa tac ctc tcc tac gac tcc agt gac cca tgc ccg ggg cag ttc acg   1396
150 Glu Tyr Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr
151          445              450              455
153 tgc cgc acg ggg cgg tgt atc cgg aag gag ctg cgc tgt gat ggc tgg   1444
154 Cys Arg Thr Gly Arg Cys Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp
155          460              465              470
157 gcc gac tgc acc gac cac agc gat gag ctc aac tgc agt tgc gac gcc   1492
158 Ala Asp Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala
159 475              480              485              490
161 ggc cac cag ttc acg tgc aag aac aag ttc tgc aag ccc ctc ttc tgg   1540
162 Gly His Gln Phe Thr Cys Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp
163              495              500              505
165 gtc tgc gac agt gtg aac gac tgc gga gac aac agc gac gag cag ggg   1588
166 Val Cys Asp Ser Val Asn Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly
167          510              515              520
169 tgc agt tgt ccg gcc cag acc ttc agg tgt tcc aat ggg aag tgc ctc   1636
170 Cys Ser Cys Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu
171          525              530              535
173 tcg aaa agc cag cag tgc aat ggg aag gac gac tgt ggg gac ggg tcc   1684
174 Ser Lys Ser Gln Gln Cys Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser
175          540              545              550
177 gac gag gcc tcc tgc ccc aag gtg aac gtc gtc act tgt acc aaa cac   1732
178 Asp Glu Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His
179 555              560              565              570
181 acc tac cgc tgc ctc aat ggg ctc tgc ttg agc aag ggc aac cct gag   1780
182 Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu
183              575              580              585
185 tgt gac ggg aag gag gac tgt agc gac ggc tca gat gag aag gac tgc   1828
186 Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys
187          590              595              600
189 gac tgt ggg ctg cgg tca ttc acg aga cag gct cgt gtt gtt ggg ggc   1876
190 Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly
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193 acg gat gcg gat gag ggc gag tgg ccc tgg cag gta agc ctg cat gct  1924
194 Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala
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197 ctg ggc cag ggc cac atc tgc ggt gct tcc ctc atc tct ccc aac tgg  1972
198 Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp
199 635             640             645             650
201 ctg gtc tct gcc gca cac tgc tac atc gat gac aga gga ttc agg tac  2020
202 Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr
203             655             660             665
205 tca gac ccc acg cag tgg acg gcc ttc ctg ggc ttg cac gac cag agc  2068
206 Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser
207             670             675             680
209 cag cgc agc gcc cct ggg gtg cag gag cgc agg ctc aag cgc atc atc  2116
210 Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile
211             685             690             695
213 tcc cac ccc ttc ttc aat gac ttc acc ttc gac tat gac atc gcg ctg  2164
214 Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu
215     700             705             710
217 ctg gag ctg gag aaa ccg gca gag tac agc tcc atg gtg cgg ccc atc  2212
218 Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met Val Arg Pro Ile
219 715             720             725             730
221 tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc ggc aag gcc atc tgg  2260
222 Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp
223             735             740             745
225 gtc acg ggc tgg gga cac acc cag tat gga ggc act ggc gcg ctg atc  2308
226 Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile
227             750             755             760
229 ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac  2356
230 Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn
231             765             770             775
233 ctc ctg ccg cag cag atc acg ccg cgc atg atg tgc gtg ggc ttc ctc  2404
234 Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu
235     780             785             790
237 agc ggc ggc gtg gac tcc tgc cag ggt gat tcc ggg gga ccc ctg tcc  2452
238 Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser
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243             815             820             825
245 gga gac ggc tgc gct cag agg aac aag cca ggc gtg tac aca agg ctc  2548
246 Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu
247             830             835             840
249 cct ctg ttt cgg gac tgg atc aaa gag aac act ggg gta ta ggggccgggg 2599
250 Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val
251     845             850             855
253 ccacccaaat gtgtacacct gcggggccac ccatcgtcca ccccagtgtg cacgcctgca 2659
254 ggctggagac tggaccgctg actgcaccag cgcccccaga acatacactg tgaactcaat 2719
255 ctccagggct ccaaatctgc ctagaaaacc tctcgcttcc tcagcctcca aagtggagct 2779
256 gggaggtaga aggggaggac actggtggtt ctactgaccc aactgggggc aaaggtttga 2839
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Input Set : **A:\1625seq.001**
Output Set: **N:\CRF4\08112003\J612466.raw**

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257 agacacagcc tcccccgcca gccccaagct gggccgaggc gcgtttgtgt atatctgcct 2899
258 cccctgtctg taaggagcag cgggaacgga gcttcggagc ctcctcagtg aaggtggtgg 2959
259 ggctgccgga tctgggctgt ggggcccttg ggccacgctc ttgaggaagc ccaggctcgg 3019
260 aggaccctgg aaaacagacg ggtctgagac tgaaattgtt ttaccagctc ccagggtgga 3079
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262 aaaaaaaa                                                         3147
264 <210> SEQ ID NO: 2
265 <211> LENGTH: 855
266 <212> TYPE: PRT
267 <213> ORGANISM: Homo Sapien
269 <400> SEQUENCE: 2
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274 Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
275          35                  40                  45
276 Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
277      50                  55                  60
278 Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
279 65                  70                  75                  80
280 Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
281              85                  90                  95
282 Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
283              100                 105                 110
284 Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
285          115                 120                 125
286 Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
287      130                 135                 140
288 Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
289 145                 150                 155                 160
290 Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
291              165                 170                 175
292 Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
293              180                 185                 190
294 Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
295          195                 200                 205
296 Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
297      210                 215                 220
298 Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
299 225                 230                 235                 240
300 His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
301              245                 250                 255
302 Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
303              260                 265                 270
304 Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
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      Pro Ser Ala Leu Pro Ile Cys Leu His Pro Ala Gly Ile Pro Pro Gly
              35                  40                  45
      Ala Ser Cys Trp Val Leu Gly Trp Lys Glu Pro Gln Asp Arg Val Pro
              50                  55                  60
      Val Ala Ala Ala Val Ser Ile Leu Thr Gln Arg Ile Cys Asp Cys Leu
      65                  70                  75                  80
      Tyr Gln Gly Ile Leu Pro Pro Gly Thr Leu Cys Val Leu Tyr Ala Glu
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      Gly Gln Glu Asn Arg Cys Glu
                      100
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*which response is the valid one?*

*If it is "Artificial Sequence" include <220>-<223> section and explanation of source material on <223> line*

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<212> TYPE: PRT
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      <213> Homo Sapien
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                  20                  25                  30
      Phe Phe Pro Leu Gln
              35
```

*same error*